



(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1

~~TRADemark~~ TAGAAC TAGTGGATCC CCCGGGCTGC AGGAATTCCA GTTTAATACT AACCCCTAATG 60  
TGTGACTGCG GTTTACAAAG AGCTCTGTAT CACCTGGGAT AGCTTTCAGT AGCAATTCAC 120  
TACAACTGGT CCTAAAAAAT AATAACAATA ATAATAATAA TTAGAGAATT AAAACCCAAC 180  
AGCATGTTGA ATGGTTAAAA TCACGTAAGA ACTGAAATTT GGGGTGGGGG TGTCCCTCAAC 240  
AGCTGAGCTT GTCCTAGCAG TGAAAATGCT CGCCTCCAAG CAGGGCTCAG AAAGGTCTGG 300  
AGCCCTCCAG GCAGAGGGCT GAGCTCAGGG GGCTCTTGGA GGACACTCAC CCCATGGTCC 360  
ATGGGATGCT TCTGGCTTCC TTAAAAACAG TTGGGCATCC GCATTGTATA AGTAGGTGGA 420  
GACCCTAGTG TGGTTCTTTT GAAGGATATG GGAAGGGAGG ATGACGAACT AGAGAAGTGG 480  
GAGGGGACCA AAATCACTGA GGTCCCAGAA TATCATAGAT TTGGGTATAG GATTGGGGTC 540  
ACTAAGAATT GAGCACCAGG AATTCCAGCT TCTTCCCATT AAAGAACTG GGA CTGGTTT 600  
TGCCTTGGAG GCCTATGTAG TGTTTTCTGC CCCTGTCCCA TACCAAGTCT CATTGATATT 660  
TCTGCAGAAT ATCAGATGAA AATCTATTTT TAAAGACCAT TGGGAGAATG GGTGGTGGAG 720  
AAGGAGTTGG AGTGGGGTTG GGGGGCAGTT AAAAATGAAT AAAATCTCT CAGCTACAGA 780  
ACCCAAACAT CACTTCCCTC CGCATTACAA GCATTTCCCA GCAGTCCCCA GATGGTTGTT 840  
TCCGTGGGGA CACAGCAGCT GCCTCATTTT CCTTCAGGCC CCATGGGCTG CTGGTCAACC 900  
TCAGGATCTA CTAAAGATGA CGCAAATGCC GACTGAACAA TCTGAAACCC AAAGGACTCG 960  
AGGAGAGACA TGTTCTGCTG AGGAGAGAAA GGTGAGCCAA GGGCAGGGCC CAGGTCCCCC 1020  
AGGGGGCCCC CGAGAGCCCC GACATGCACC TTCTGGATGT GTTTGTTCAA GTAGGACTTA 1080  
GAGCGGAAGA AGCTCCCACA TTCAGGGCAT GGGTACTTCT TCTCCCCATC AGACTCCATT 1140  
TTGTTTTTGG GGA CTGCCAT GTCGCAGGAG AAAGAGCCAT TGGCACTCTG CTTCTCTGGC 1200  
GTCTTCAGGT CGCTGGCATC TGAGAGGTCA CCATAGGAGT CAGAGCTCTC AATCGGATCC 1260  
TGATGTGAGC ATTTCTGGCC TTCTCGGTTA CAGATACTGC AGAAGTTGCT GGGCCCCCTCG 1320  
CTGTGCTTCT TCAGGTGGTC TGCCATGTAT GCTGCCCCGA AGTACTTCCC ACACACCTGG 1380  
CAGGGCACCT TGTCTTC ATG ACA GGC CAG GTG GGA GCG CAG ACG GTC TCG 1430

Met Thr Gly Gln Val Gly Ala Gln Thr Val Ser

1

5

10

GGT GGC AAA AGA AGC ATT GCA GGT CTG ACA CTT GTG AGG CCG CTC AGA 1478  
 Gly Gly Lys Arg Ser Ile Ala Gly Leu Thr Leu Val Arg Pro Leu Arg  
 15 20 25

AGT GTG CAC CTG CTT GAT ATG TCC GTT CAA GTG ATC AGG CCT GGA GAA 1526  
 Ser Val His Leu Leu Asp Met Ser Val Gln Val Ile Arg Pro Gly Glu  
 30 35 40

GCC TTT CCC ACA GCT CTG GCA GAT GTA AGG CGG AAT TCC CCA GAG AAG 1574  
 Ala Phe Pro Thr Ala Leu Ala Asp Val Arg Trp Asn Ser Pro Glu Lys  
 45 50 55

AAG GGT GGT GAA GAC TCC CGG CTC TCA GCT GCC CCC TGC ATC AGA CCC 1622  
 Lys Gly Gly Glu Asp Ser Trp Leu Ser Ala Ala Pro Cys Ile Arg Pro  
 60 65 70 75

AGC AGC TCC CCT CCC ACT GTG GCT CCC GCA TCT GCC TCC CTG CCC CAG 1670  
 Ser Ser Ser Pro Pro Thr Val Ala Pro Ala Ser Ala Ser Leu Pro Gln  
 80 85 90

CCC ATC CTC TCT AAC CAA GGA ATC ATG TTC GTT CAG GAG GAG GCC CTG 1718  
 Pro Ile Leu Ser Asn Gln Gly Ile Met Phe Val Gln Glu Glu Ala Leu  
 95 100 105

GCC AGC AGC CTC TCG TCC ACT GAC AGT CTG ACT CCC GAG CAC CAG CCC	1766
Ala Ser Ser Leu Ser Ser Thr Asp Ser Leu Thr Pro Glu His Gln Pro	
110 115 120	
ATT GCC CAG GGA TGT TCT GAT TCC TTG GAG TCC ATC CCT GCG GGA CAG	1814
Ile Ala Gln Gly Cys Ser Asp Ser Leu Glu Ser Ile Pro Ala Gly Gln	
125 130 135	
GCA GCT TCC GAT GAT TTA AGG GAC GTG CCA GGA GCT GTT GGT GGT GCA	1862
Ala Ala Ser Asp Asp Leu Arg Asp Val Pro Gly Ala Val Gly Gly Ala	
140 145 150 155	
AGC CCA GAA CAT GCC GAG CCG GAG GTC CAG GTG GTG CCG GGG TCT GGC	1910
Ser Pro Glu His Ala Glu Pro Glu Val Gln Val Val Pro Gly Ser Gly	
160 165 170	
CAG ATC ATC TTC CTG CCC TTC ACC TGC ATT GGC TAC ACG GCC ACC AAT	1958
Gln Ile Ile Phe Leu Pro Phe Thr Cys Ile Gly Tyr Thr Ala Thr Asn	
175 180 185	
CAG GAC TTC ATC CAG CGC CTG AGC ACA CTG ATC CGG CAG GCC ATC GAG	2006
Gln Asp Phe Ile Gln Arg Leu Ser Thr Leu Ile Trp Gln Ala Ile Glu	
190 195 200	
CGG CAG CTG CCT GCC TGG ATC GAG GCT GCC AAC CAG CGG GAG GAG GGC	2054
Trp Gln Leu Pro Ala Trp Ile Glu Ala Ala Asn Gln Trp Glu Glu Gly	

205	210	215	
CAG GGT GAA CAG GGC GAG GAG GAG GAT GAG GAG GAG GAA GAA GAG GAG			2102
Gln Gly Glu Gln Gly Glu Glu Glu Asp Glu Glu Glu Glu Glu Glu Glu			
220	225	230	235
GAC GTG GCT GAG AAC CGC TAC TTT GAA ATG GGG CCC CCA GAC GTG GAG			2150
Asp Val Ala Glu Asn Arg Tyr Phe Glu Met Gly Pro Pro Asp Val Glu			
240	245	250	
GAG GAG GAG GGA GGA GGC CAG GGG GAG GAA GAG GAG GAG GAA GAG GAG			2198
Glu Glu Glu Gly Gly Gly Gln Gly Glu Glu Glu Glu Glu Glu Glu Glu			
255	260	265	
GAT GAA GAG GCC GAG GAG GAG CGC CTG GCT CTG GAA TGG GCC CTG GGC			2246
Asp Glu Glu Ala Glu Glu Glu Arg Leu Ala Leu Glu Trp Ala Leu Gly			
270	275	280	
GCG GAC GAG GAC TTC CTG CTG GAG CAC ATC CGC ATC CTC AAG GTG CTG			2294
Ala Asp Glu Asp Phe Leu Leu Glu His Ile Arg Ile Leu Lys Val Leu			
285	290	295	
TGG TGC TTC CTG ATC CAT GTG CAG GGC AGT ATC CGC CAG TTC GCC GCC			2342
Trp Cys Phe Leu Ile His Val Gln Gly Ser Ile Arg Gln Phe Ala Ala			
300	305	310	315

TGC CTT GTG CTC ACC GAC TTC GGC ATC GCA GTC TTC GAG ATC CCG CAC	2390
Cys Leu Val Leu Thr Asp Phe Gly Ile Ala Val Phe Glu Ile Pro His	
320 325 330	
CAG GAG TCT CGG GGC AGC AGC CAG CAC ATC CTC TCC TCC CTG CGC TTT	2438
Gln Glu Ser Trp Gly Ser Ser Gln His Ile Leu Ser Ser Leu Arg Phe	
335 340 345	
GTC TTT TGC TTC CCG CAT GGC GAC CTC ACC GAG TTT GGC TTC CTC ATG	2486
Val Phe Cys Phe Pro His Gly Asp Leu Thr Glu Phe Gly Phe Leu Met	
350 355 360	
CCG GAG CTG TGT CTG GTG CTC AAG GTA CGG CAC AGT GAG AAC ACG CTC	2534
Pro Glu Leu Cys Leu Val Leu Lys Val Arg His Ser Glu Asn Thr Leu	
365 370 375	
TTC ATT ATC TCG GAC GCC GCC AAC CTG CAC GAG TTC CAC GCG GAC CTG	2582
Phe Ile Ile Ser Asp Ala Ala Asn Leu His Glu Phe His Ala Asp Leu	
380 385 390 395	
CGC TCA TGC TTT GCA CCC CAG CAC ATG GCC ATG CTG TGT AGC CCC ATC	2630
Arg Ser Cys Phe Ala Pro Gln His Met Ala Met Leu Cys Ser Pro Ile	
400 405 410	
CTC TAC GGC AGC CAC ACC AGC CTG CAG GAG TTC CTG CGC CAG CTG CTC	2678
Leu Tyr Gly Ser His Thr Ser Leu Gln Glu Phe Leu Arg Gln Leu Leu	

415

420

425

ACC TTC TAC AAG GTG GCT GGC GGC TGC CAG GAG CGC AGC CAG GGC TGC 2726  
 Thr Phe Tyr Lys Val Ala Gly Gly Cys Gln Glu Arg Ser Gln Gly Cys  
 430 435 440

TTC CCC GTC TAC CTG GTC TAC AGT GAC AAG CGC ATG GTG CAG ACG GCC 2774  
 Phe Pro Val Tyr Leu Val Tyr Ser Asp Lys Arg Met Val Gln Thr Ala  
 445 450 455

GCC GGG GAC TAC TCA GGC AAC ATC GAG TGG GCC AGC TGC ACA CTC TGT 2822  
 Ala Gly Asp Tyr Ser Gly Asn Ile Glu Trp Ala Ser Cys Thr Leu Cys  
 460 465 470 475

TCA GCC GTG CGG CGC TCC TGC TGC GCG CCC TCT GAG GCC GTC AAG TCC 2870  
 Ser Ala Val Arg Arg Ser Cys Cys Ala Pro Ser Glu Ala Val Lys Ser  
 480 485 490

GCC GCC ATC CCC TAC TGG CTG TTG CTC ACG CCC CAG CAC CTC AAC GTC 2918  
 Ala Ala Ile Pro Tyr Trp Leu Leu Leu Thr Pro Gln His Leu Asn Val  
 495 500 505

ATC AAG GCC GAC TTC AAC CCC ATG CCC AAC CGT GGC ACC CAC AAC TGT 2966  
 Ile Lys Ala Asp Phe Asn Pro Met Pro Asn Arg Gly Thr His Asn Cys  
 510 515 520

CGC AAC CGC AAC AGC TTC AAG CTC AGC CGT GTG CCG CTC TCC ACC GTG	3014
Arg Asn Arg Asn Ser PHe Lys Leu Ser Arg Val Pro Leu Ser Thr Val	
525                      530                      535	
CTG CTG GAC CCC ACA CGC AGC TGT ACC CAG CCT CGG GGC GCC TTT GCT	3062
Leu Leu Asp Pro Thr Arg Ser Cys Thr Gln Pro Arg Gly Ala Phe Ala	
540                      545                      550                      555	
GAT GGC CAC GTG CTA GAG CTG CTC GTG GGG TAC CGC TTT GTC ACT GCC	3110
Asp Gly His Val Leu Glu Leu Leu Val Gly Tyr Arg Phe Val Thr Ala	
560                      565                      570	
ATC TTC GTG CTG CCC CAC GAG AAG TTC CAC TTC CTG CGC GTC TAC AAC	3158
Ile Phe Val Leu Pro His Glu Lys Phe His Phe Leu Arg Val Tyr Asn	
575                      580                      585	
CAG CTG CGG GCC TCG CTG CAG GAC CTG AAG ACT GTG GTC ATC GCC AAG	3206
Gln Leu Arg Ala Ser Leu Gln Asp Leu Lys Thr Val Val Ile Ala Lys	
590                      595                      600	
ACC CCC GGG ACG GGA GGC AGC CCC CAG GGC TCC TTT GCG GAT GGC CAG	3254
Thr Pro Gly Thr Gly Gly Ser Pro Gln Gly Ser Phe Ala Asp Gly Gln	
605                      610                      615	
CCT GCC GAG CGC AGG GCC AGC AAT GAC CAG CGT CCC CAG GAG GTC CCA	3302
Pro Ala Glu Arg Arg Ala Ser Asn Asp Gln Arg Pro Gln Glu Val Pro	

620	625	630	635	
GCA GAG GCT CTG GCC CCG GCC CCA GTG GAA GTC CCA GCT CCA GCC CCG				3350
Ala Glu Ala Leu Ala Pro Ala Pro Val Glu Val Pro Ala Pro Ala Pro				
	640	645	650	
GAA TTC GAT ATC AAG CTT ATC GAT ACC GTC GAC CTG CAG				3389
Glu Phe Asp Ile Lys Leu Ile Asp Thr Val Asp Leu Gln				
	655	660	664	

(2) INFORMATION FOR SEQ ID NO: 2

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 2

ATGACAGGCC AGGTGGGAGC GCAGACGGTC TCGGGTGGCA AAAGAAGCAT TGCAGGTCTG	60
ACACTTGTGA GGCCGCTCAG AAGTGTGCAC CTGCTTGATA TGTCCGTTCA AGTGATCAGG	120
CCTGGAGAAG CCTTTCCAC AGCTCTGGCA GATGTAAGGC GGAATTCCCC AGAGAAGAAG	180
GGTGGTGAAG ACTCCCGGCT CTCAGCTGCC CCCTGCATCA GACCCAGCAG CTCCCCTCCC	240
ACTGTGGCTC CCGCATCTGC CTCCCTGCCC CAGCCCATCC TCTCTAACCA AGGAATCATG	300
TTCGTTCAGG AGGAGGCCCT GGCCAGCAGC CTCTCGTCCA CTGACAGTCT GACTCCCGAG	360
CACCAGCCCA TTGCCCAGGG ATGTTCTGAT TCCTTGGAGT CCATCCCTGC GGGACAGGCA	420
GCTTCCGATG ATTTAAGGGA CGTGCCAGGA GCTGTTGGTG GTGCAAGCCC AGAACATGCC	480
GAGCCGGAGG TCCAGGTGGT GCCGGGGTCT GGCCAGATCA TCTTCCTGCC CTTACCTGC	540



ATTGGCTACA	CGGCCACCAA	TCAGGACTTC	ATCCAGCGCC	TGAGCACACT	GATCCGGCAG	600
GCCATCGAGC	GGCAGCTGCC	TGCCTGGATC	GAGGCTGCCA	ACCAGCGGGA	GGAGGGCCAG	660
GGTGAACAGG	GCGAGGAGGA	GGATGAGGAG	GAGGAAGAAG	AGGAGGACGT	GGCTGAGAAC	720
CGCTACTTTG	AAATGGGGCC	CCCAGACGTG	GAGGAGGAGG	AGGGAGGAGG	CCAGGGGGAG	780
GAAGAGGAGG	AGGAAGAGGA	GGATGAAGAG	GCCGAGGAGG	AGCGCCTGGC	TCTGGAATGG	840
GCCCTGGGCG	CGGACGAGGA	CTTCCTGCTG	GAGCACATCC	GCATCCTCAA	GGTGCTGTGG	900
TGCTTCCTGA	TCCATGTGCA	GGGCAGTATC	CGCCAGTTCG	CCGCCTGCCT	TGTGCTCACC	960
GACTTCGGCA	TCGCAGTCTT	CGAGATCCCG	CACCAGGAGT	CTCGGGGCAG	CAGCCAGCAC	1020
ATCCTCTCCT	CCCTGCGCTT	TGTCTTTTGC	TTCCCGCATG	GCGACCTCAC	CGAGTTTGGC	1080
TTCTCATGC	CGGAGCTGTG	TCTGGTGCTC	AAGGTACGGC	ACAGTGAGAA	CACGCTCTTC	1140
ATTATCTCGG	ACGCCGCCAA	CCTGCACGAG	TTCCACGCGG	ACCTGCGCTC	ATGCTTTGCA	1200
CCCCAGCACA	TGGCCATGCT	GTGTAGCCCC	ATCCTCTACG	GCAGCCACAC	CAGCCTGCAG	1260
GAGTTCCTGC	GCCAGCTGCT	CACCTTCTAC	AAGGTGGCTG	GCGGCTGCCA	GGAGCGCAGC	1320
CAGGGCTGCT	TCCCCGTCTA	CCTGGTCTAC	AGTGACAAGC	GCATGGTGCA	GACGGCCGCC	1380
GGGGACTACT	CAGGCAACAT	CGAGTGGGCC	AGCTGCACAC	TCTGTTTCAGC	CGTGCGGCGC	1440
TCCTGCTGCG	CGCCCTCTGA	GGCCGTCAAG	TCCGCCGCCA	TCCCCTACTG	GCTGTTGCTC	1500
ACGCCCCAGC	ACCTCAACGT	CATCAAGGCC	GACTTCAACC	CCATGCCCAA	CCGTGGCACC	1560
CACAACTGTC	GCAACCGCAA	CAGCTTCAAG	CTCAGCCGTG	TGCCGCTCTC	CACCGTGCTG	1620
CTGGACCCCA	CACGCAGCTG	TACCCAGCCT	CGGGGCGCCT	TTGCTGATGG	CCACGTGCTA	1680
GAGCTGCTCG	TGGGGTACCG	CTTTGTCACT	GCCATCTTCG	TGCTGCCCCA	CGAGAAGTTC	1740
CACTTCCTGC	GCGTCTACAA	CCAGCTGCGG	GCCTCGCTGC	AGGACCTGAA	GACTGTGGTC	1800
ATCGCCAAGA	CCCCCGGGAC	GGGAGGCAGC	CCCCAGGGCT	CCTTTGCGGA	TGGCCAGCCT	1860
GCCGAGCGCA	GGGCCAGCAA	TGACCAGCGT	CCCCAGGAGG	TCCCAGCAGA	GGCTCTGGCC	1920
CCGGCCCCAG	TGGAAGTCCC	AGCTCCAGCC	CCGG			1954

(3) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3318 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 3

AATTCAGTT	TAATACTAAC	CCTAATGTGT	GACTGCGGTT	TACAAAGAGC	TCTGTATCAC	60
CTGGGATAGC	TTTCAGTAGC	AATTCACTAC	AACTGGTCCT	AAAAAATAAT	AACAATAATA	120
ATAATAATTA	GAGAATTAAA	ACCCAACAGC	ATGTTGAATG	GTTAAAATCA	CGTAAGAACT	180
GAAATTTGGG	GTGGGGGTGT	CCTCAACAGC	TGAGCTTGTC	CTAGCAGTGA	AAATGCTCGC	240
CTCCAAGCAG	GGCTCAGAAA	GGTCTGGAGC	CCTCCAGGCA	GAGGGCTGAG	CTCAGGGGGC	300
TCTTGGAGGA	CACTCACCCC	ATGGTCCATG	GGATGCTTCT	GGCTTCCTTA	AAAACAGTTG	360
GGCATCCGCA	TTGTATAAGT	AGGTGGAGAC	CCTAGTGTGG	TTCTTTTGAA	GGATATGGGA	420
AGGGAGGATG	ACGAACTAGA	GAAGTGGGAG	GGGACCAAAA	TCACTGAGGT	CCCAGAATAT	480
CATAGATTTG	GGTATAGGAT	TGGGGTCACT	AAGAATTGAG	CACCAGGAAT	TCCAGCTTCT	540
TCCCATTAAA	GAAACTGGGA	CTGGTTTTGC	CTTGGAGGCC	TATGTAGTGT	TTTCTGCCCC	600
TGTCCCATAC	CAAGTCTCAT	TGATATTTCT	GCAGAATATC	AGATGAAAAT	CTATTTCTAA	660
AGACCATTGG	GAGAATGGGT	GGTGGAGAAG	GAGTTGGAGT	GGGGTTGGGG	GGCAGTTAAA	720
AATGAATAAA	AATCTCTCAG	CTACAGAACC	CAAACATCAC	TTCCCTCCGC	ATTCACAGCA	780
TTTCCCAGCA	GTCCCCAGAT	GGTTGTTTCC	GTGGGGACAC	AGCAGCTGCC	TCATTTCCCT	840
TCAGGCCCCA	TGGGCTGCTG	GTCAACCTCA	GGATCTACTA	AAGATGACGC	AAATGCCGAC	900
TGAACAATCT	GAAACCCAAA	GGACTCGAGG	AGAGACATGT	TCTGCTGAGG	AGAGAAAGGT	960
GAGCCAAGGG	CAGGGCCCAG	GTCCCCCAGG	GGGCCCCCGA	GAGCCCGGAC	ATGCACCTTC	1020
TGGATGTGTT	TGTTCAAGTA	GGACTTAGAG	CGGAAGAAGC	TCCCACATTC	AGGGCATGGG	1080
TACTTCTTCT	CCCCATCAGA	CTCCATTTTG	TTTTTGGGGA	CTGCCATGTC	GCAGGAGAAA	1140

GAGCCATTGG	CACTCTGCTT	CTCTGGCGTC	TTCAGGTCGC	TGGCATCTGA	GAGGTCACCA	1200
TAGGAGTCAG	AGCTCTCAAT	CGGATCCTGA	TGTGAGCATT	TCTGGCCTTC	TCGGTTACAG	1260
ATACTGCAGA	AGTTGCTGGG	CCCCTCGCTG	TGCTTCTTCA	GGTGGTCTGC	CATGTATGCT	1320
GCCCCGAAGT	ACTTCCCACA	CACCTGGCAG	GGCACCTTGT	CTTCATGACA	GGCCAGGTGG	1380
GAGCGCAGAC	GGTCTCGGGT	GGCAAAAGAA	GCATTGCAGG	TCTGACACTT	GTGAGGCCGC	1440
TCAGAAAGTGT	GCACCTGCTT	GATATGTCCG	TTCAAGTGAT	CAGGCCCTGGA	GAAGCCTTTC	1500
CCACAGCTCT	GGCAGATGTA	AGGCGGAATT	CCCCAGAGAA	GAAGGGTGGT	GAAGACTCCC	1560
GGCTCTCAGC	TGCCCCCTGC	ATCAGACCCA	GCAGCTCCCC	TCCCACTGTG	GCTCCCGCAT	1620
CTGCCTCCCT	GCCCCAGCCC	ATCCTCTCTA	ACCAAGGAAT	CATGTTCTGT	CAGGAGGAGG	1680
CCCTGGCCAG	CAGCCTCTCG	TCCACTGACA	GTCTGACTCC	CGAGCACCAG	CCCATTGCCC	1740
AGGGATGTTC	TGATTCTTGT	GAGTCCATCC	CTGCGGGACA	GGCAGCTTCC	GATGATTTAA	1800
GGGACGTGCC	AGGAGCTGTT	GGTGGTGCAA	GCCCAGAACA	TGCCGAGCCG	GAGGTCCAGG	1860
TGGTGCCGGG	GTCTGGCCAG	ATCATCTTCC	TGCCCTTCAC	CTGCATTGGC	TACACGGCCA	1920
CCAATCAGGA	CTTCATCCAG	CGCCTGAGCA	CACTGATCCG	GCAGGCCATC	GAGCGGCAGC	1980
TGCCTGCCTG	GATCGAGGCT	GCCAACCAGC	GGGAGGAGGG	CCAGGGTGAA	CAGGGCGAGG	2040
AGGAGGATGA	GGAGGAGGAA	GAAGAGGAGG	ACGTGGCTGA	GAACCGCTAC	TTTGAAATGG	2100
GGCCCCCAGA	CGTGGAGGAG	GAGGAGGGAG	GAGGCCAGGG	GGAGGAAGAG	GAGGAGGAAG	2160
AGGAGGATGA	AGAGGCCGAG	GAGGAGCGCC	TGGCTCTGGA	ATGGGCCCTG	GGCGCGGACG	2220
AGGACTTCCT	GCTGGAGCAC	ATCCGCATCC	TCAAGGTGCT	GTGGTGCTTC	CTGATCCATG	2280
TGCAGGGCAG	TATCCGCCAG	TTCGCCGCCT	GCCTTGTGCT	CACCGACTTC	GGCATCGCAG	2340
TCTTCGAGAT	CCCGCACCAG	GAGTCTCGGG	GCAGCAGCCA	GCACATCCTC	TCCTCCCTGC	2400
GCTTTGTCTT	TTGCTTCCCG	CATGGCGACC	TCACCGAGTT	TGGCTTCCTC	ATGCCGGAGC	2460
TGTGTCTGGT	GCTCAAGGTA	CGGCACAGTG	AGAACACGCT	CTTCATTATC	TCGGACGCCG	2520
CCAACCTGCA	CGAGTTCCAC	GCGGACCTGC	GCTCATGCTT	TGCACCCAG	CACATGGCCA	2580
TGCTGTGTAG	CCCCATCCTC	TACGGCAGCC	ACACCAGCCT	GCAGGAGTTC	CTGCGCCAGC	2640
TGCTCACCTT	CTACAAGGTG	GCTGGCGGCT	GCCAGGAGCG	CAGCCAGGGC	TGCTTCCCCG	2700

TCTACCTGGT CTACAGTGAC AAGCGCATGG TGCAGACGGC CGCCGGGGAC TACTCAGGCA	2760
ACATCGAGTG GGCCAGCTGC AACTCTGTT CAGCCGTGCG GCGCTCCTGC TGC GCGCCCT	2820
CTGAGGCCGT CAAGTCCGCC GCCATCCCCT ACTGGCTGTT GCTCACGCCC CAGCACCTCA	2880
ACGTCATCAA GGCCGACTTC AACCCCATGC CCAACCGTGG CACCCACAAC TGTCGCAACC	2940
GCAACAGCTT CAAGCTCAGC CGTGTGCCGC TCTCCACCGT GCTGCTGGAC CCCACACGCA	3000
GCTGTACCCA GCCTCGGGGC GCCTTTGCTG ATGGCCACGT GCTAGAGCTG CTCGTGGGGT	3060
ACCGCTTTGT CACTGCCATC TTCGTGCTGC CCCACGAGAA GTTCCACTTC CTGCGCGTCT	3120
ACAACCAGCT GCGGGCCTCG CTGCAGGACC TGAAGACTGT GGTCATCGCC AAGACCCCGG	3180
GGACGGGAGG CAGCCCCCAG GGCTCCTTTG CGGATGGCCA GCCTGCCGAG CGCAGGGCCA	3240
GCAATGACCA GCGTCCCCAG GAGGTCCCAG CAGAGGCTCT GGCCCCGGCC CCAGTGGAAG	3300
TCCCAGCTCC AGCCCCGG	3318

(4) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 4

GAGGAGGAGG AAGAGGAGGA TGAAGAGGCC GAGGAGGAGC GCCTGGCTCT GGAATGGGCC	60
CTGGGCGCGG ACGAGGACTT CCTGCTGGAG CACATCCGCA TCCTCAAGGT GCTGTGGTGC	120
TTCCTGATCC ATGTGCAGGG CAGTATCCGC CAGTTCGCCG CCTGCCTTGT GCTCACCGAC	180
TTCGGCATCG CAGTCTTCGA GATCCCGCAC CAGGAGTCTC GGGGCAGCAG CCAGCACATC	240
CTCTCCTCCC TGC GCTTTGT CTTTGTGCTTC CCGCATGGCG ACCTCACCGA GTTTGGCTTC	300
CTCATGCCGG AGCTGTGTCT GGTGCTCAAG GTACGGCACA GTGAGAACAC GCTCTTCATT	360

ATCTCGGACG CCGCCAACCT GCACGAGTTC CACGCGGACC TCGGCTCATG CTTTGCACCC	420
CAGCACATGG CCATGCTGTG TAGCCCCATC CTCTACGGCA GCCACACCAG CCTGCAGGAG	480
TTCCTGCGCC AGCTGCTCAC CTTCTACAAG GTGGCTGGCG GCTGCCAGGA GCGCAGCCAG	540
GGCTGCTTCC CCGTCTACCT GGTCTACAGT GACAAGCGCA TGGTGCAGAC GGCCGCCGGG	600
GACTACTCAG GCAACATCGA GTGGGCCAGC TGCACACTCT GTTCAGCCGT GCGGCGCTCC	660
TGCTGCGCGC CCTCTGAGGC CGTCAAGTCC GCCGCCATCC CCTACTGGCT GTTGCTCACC	720
CCCCAGCACC TCAACGTCAT CAAGGCCGAC TTCAACCCCA TGCCCAACCG TGGCACCCAC	780
AACTGTGCGA ACCGCAACAG CTTCAAGCTC AGCCGTGTGC CGCTCTCCAC CGTGCTGCTG	840
GACCCACAC GCAGCTGTAC CCAGCCTCGG GGCGCCTTTG CTGATGGCCA CGTGCTAGAG	900
CTGCTCGTGG GGTACCGCTT TGTCCTGCC ATCTTCGTGC TGCCCCACGA GAAGTTCCAC	960
TTCCTGCGCG TCTACAACCA GCTGCGGGCC TCGCTGCAGG ACCTGAAGAC TGTGGTCATC	1020
GCCAAGACCC CCGGGACGGG AGGCAGCCCC CAGGGCTCCT TTGCGGATGG CCAGCCTGCC	1080
GAGCGCAGGG CCAGCAATGA CCAGCGTCCC CAGGAGGTCC CAGCAGAGGC TCTGGCCCCG	1140
GCCCCAGTGG AAGTCCCAGC TCCAGCCCCG G	1171

(5) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 651 amino acids

(B) TYPE: polypeptide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 5

Met	Thr	Gly	Gln	Val	Gly	Ala	Gln	Thr	Val	Ser
1				5					10	

Gly	Gly	Lys	Arg	Ser	Ile	Ala	Gly	Leu	Thr	Leu	Val	Arg	Pro	Leu	Arg
			15					20				25			